

00632722000400

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(-40)
1
Met Gly Arg Pro Leu His Leu Val Leu Leu Ser Ala Ser Leu Ala Gly Leu Leu Leu
ATG GGG CGC CCA CTG CAC CTC GTC CTG CTC AGT GCC TCC CTG GCT GGC CTC CTG CTG
          9              18              27              36              45              54

(-4) (-1)
40
Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn Asn Ile Leu Ala Arg Val Thr Arg
CTC GGG GAA AGT CTG TTC ATC CGC AGG GAG CAG GCC AAC AAC ATC CTG GCG AGG GTC ACG AGG
          66              75              84              93              102              111              120

(+1)
41
Ala Asn Ser Phe Leu Glu Glu Met Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr
GCC AAT TCC TTT CTT GAA GAG ATG AAG AAA GGA CAC CTC GAA AGA GAG TGC GAG GAA GAG ACC
          129              138              147              156              165              174              183

Cys Ser Tyr Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe Trp Asn
TGC TCA TAC GAA GAG GCC CGC GAG GTC TTT GAG GAC AGC GAC AAG ACG AAT GAA TTC TGG AAT
          192              201              210              219              228              237              246

Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln Asn Gln Gly Lys Cys Lys Asp
AAA TAC AAA GAT GGC GAC CAG TGT GAG ACC AGT CCT TGC CAG AAC CAG GGC AAA TGT AAA GAC
          255              264              273              282              291              300              309

Gly Leu Gly Glu Tyr Thr Cys Thr Cys Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe
GGC CTC GGG GAA TAC ACC TGC ACC TGT TTA GAA GGA TTC GAA GGC AAA AAC TGT GAA TTA TTC
          318              327              336              345              354              363              372

Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln Asn
ACA CGG AAG CTC TGC AGC CTG GAC AAC GGG GAC TGT GAC CAG TTC TGC CAC GAG GAA CAG AAC
          381              390              399              408              417              426              435

Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn Gly Lys Ala Cys Ile Pro
TCT GTG GTG TGC TCC TGC GCC CGC GGG TAC ACC CTG GCT GAC AAC GGC AAG GCC TGC ATT CCC
          444              453              462              471              480              489              498

178 179 180 181 182 183
Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala
ACA GGG CCC TAC CCC TGT GGG AAA CAG ACC CTG GAA CGC AGG AAG AGG TCA GTG GCC CAG GCC
          507              516              525              534              543              552              561

Thr Ser Ser Ser Gly Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
ACC AGC AGC AGC GGG GAG GCC CCT GAC AGC ATC ACA TGG AAG CCA TAT GAT GCA GCC GAC CTG
          570              579              588              597              606              615              624

R6
229
Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln Pro Glu Arg Gly Asp
GAC CCC ACC GAG AAC CCC TTC GAC CTG CTT GAC TTC AAC CAG ACG CAG CCT GAG AGG GGC GAC
          633              642              651              660              669              678              687

R5 R4 R3 R2 R1
234 235
Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala
AAC AAC CTC ACC AGG ATC GTG GGA GGC CAG GAA TGC AAG GAC GGG GAG TGT CCC TGG CAG GCC
          696              705              714              723              732              741              750

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Fig. 1-1

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Leu Leu Ile Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile
 CTG CTC ATC AAT GAG GAA AAC GAG GGT TTC TGT GGT GGA ACT ATT CTG AGC GAG TTC TAC ATC
 759 768 777 786 795 804 813

Leu Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg Asn
 CTA ACG GCA GCC CAC TGT CTC TAC CAA GCC AAG AGA TTC AAG GTG AGG GTA GGG GAC CGG AAC
 822 831 840 849 858 867 876

Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val Val Ile Lys His Asn Arg
 ACG GAG CAG GAG GAG GGC GGT GAG GCG GTG CAC GAG GTG GAG GTG GTC ATC AAG CAC AAC CGG
 885 894 903 912 921 930 939

Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe
 TTC ACA AAG GAG ACC TAT GAC TTC GAC ATC GCC GTG CTC CGG CTC AAG ACC CCC ATC ACC TTC
 948 957 966 975 984 993 1002

Arg Met Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr
 CGC ATG AAC GTG GCG CCT GCC TGC CTC CCC GAG CGT GAC TGG GCC GAG TCC ACG CTG ATG ACG
 1011 1020 1029 1038 1047 1056 1065

Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly Arg Gln Ser Thr Arg
 CAG AAG ACG GGG ATT GTG AGC GGC TTC GGG CGC ACC CAC GAG AAG GGC CGG CAG TCC ACC AGG
 1074 1083 1092 1101 1110 1119 1128

Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile
 CTC AAG ATG CTG GAG GTG CCC TAC GTG GAC CGC AAC AGC TGC AAG CTG TCC AGC AGC TTC ATC
 1137 1146 1155 1164 1173 1182 1191

Ile Thr Gln Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp
 ATC ACC CAG AAC ATG TTC TGT GCC GGC TAC GAC ACC AAG CAG GAG GAT GCC TGC CAG GGC GAC
 1200 1209 1218 1227 1236 1245 1254

Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val Ser Trp
 AGC GGG GGC CCG CAC GTC ACC CGC TTC AAG GAC ACC TAC TTC GTG ACA GGC ATC GTC AGC TGG
 1263 1272 1281 1290 1299 1308 1317

Gly Glu Ser Cys Ala Arg Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys
 GGA GAG AGC TGT GCC CGT AAG GGG AAG TAC GGG ATC TAC ACC AAG GTC ACC GCC TTC CTC AAG
 1326 1335 1344 1353 1362 1371 1380

469 470 475 476 480
 Trp Ile Asp Arg Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu Val
 TGG ATC GAC AGG TCC ATG AAA ACC AGG GGC TTG CCC AAG GCC AAG AGC CAT GCC CCG GAG GTC
 1389 1398 1407 1416 1425 1434 1443

488
 Ile Thr Ser Ser Pro Leu Lys TER
 ATA ACG TCC TCT CCA TTA AAG TGA
 1452 1461 1467

Pre-/Propeptid
 'Connecting' Tripeptide
 Activation Peptide

Fig. 1-2

The diagram illustrates the activation of Factor IX (fIX) to Factor IXa (fIXa) and the subsequent activation of Factor X (fX) to Factor Xa (fXa) by Factor IXa.

Factor IX (fIX) and Factor IXa (fIXa): The structure of fIX is shown as a single chain with a Light Chain and a Heavy Chain. The Activation Peptide is located between the Light Chain and the Heavy Chain. The sequence of the Activation Peptide is QSFNDFTR. The activation of fIX to fIXa is catalyzed by fIXa, which cleaves the Activation Peptide at the site indicated by the arrow (between T and R).

Factor X (fX) and Factor Xa (fXa): The structure of fX is shown as a single chain with a Light Chain and a Heavy Chain. The Activation Peptide is located between the Light Chain and the Heavy Chain. The sequence of the Activation Peptide is RGDNNLTR. The activation of fX to fXa is catalyzed by fVIIa/TF or fIXa/fVIIIa, which cleave the Activation Peptide at the site indicated by the arrow (between T and R).

Factor IXa (fIXa) and Factor Xa (fXa): The structure of fIXa is shown as a single chain with a Light Chain and a Heavy Chain. The Activation Peptide is located between the Light Chain and the Heavy Chain. The sequence of the Activation Peptide is QSFNDFTR. The activation of fIXa to fIXa is catalyzed by fIXa, which cleaves the Activation Peptide at the site indicated by the arrow (between T and R).

Fig. 2

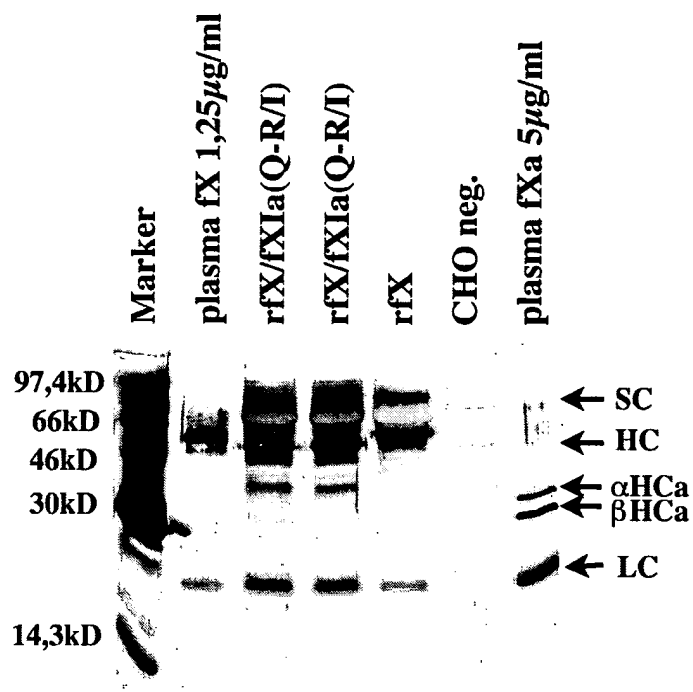


Fig. 3

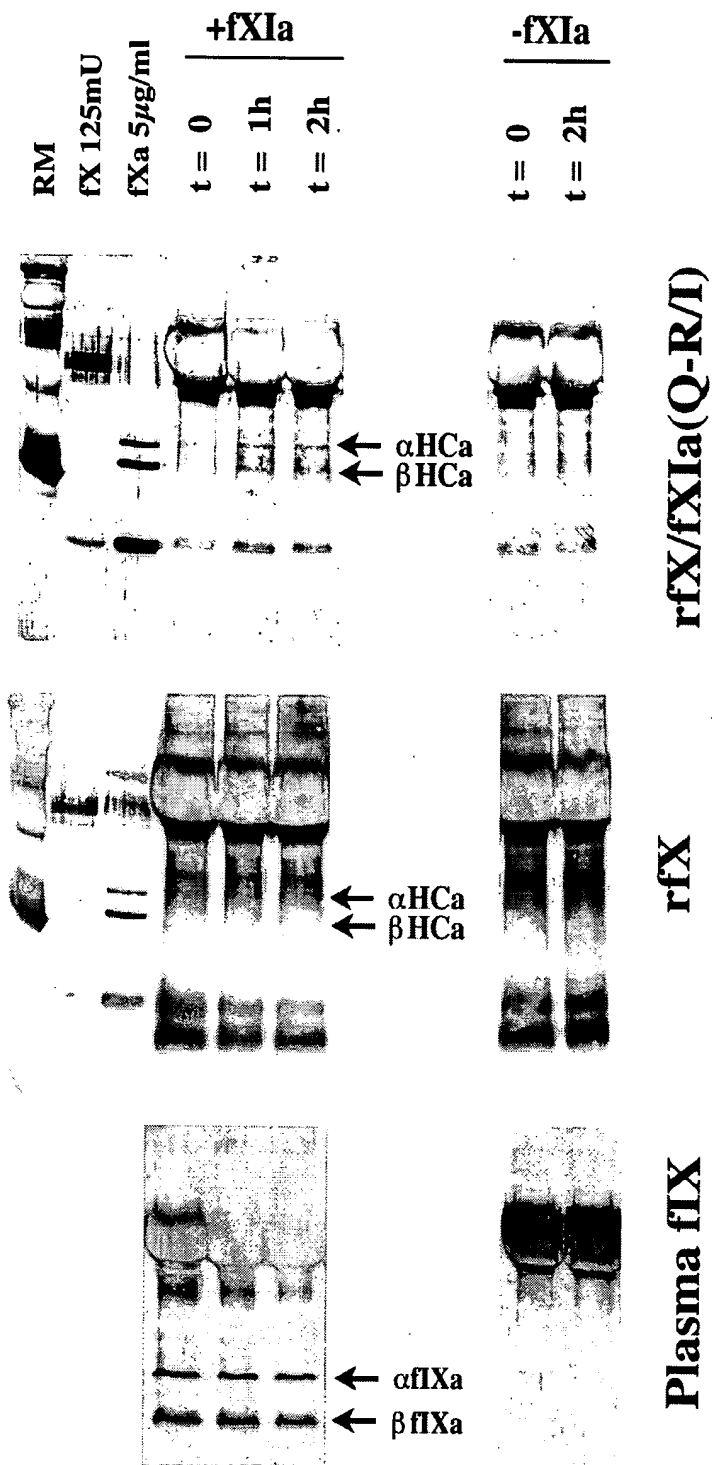


Fig. 4

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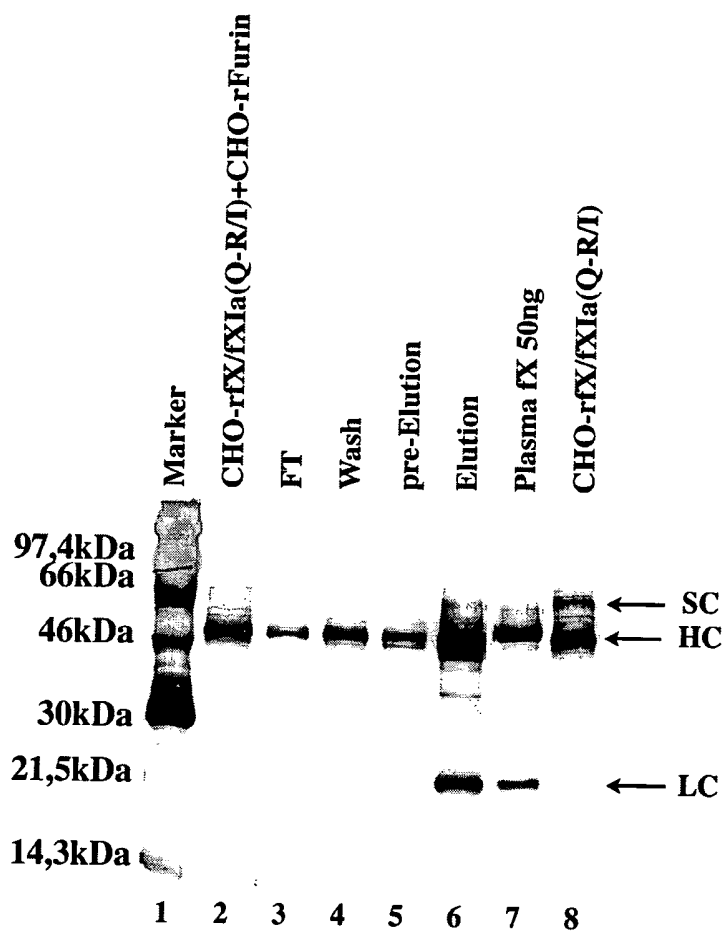


Fig. 5